SEQUENCE LISTING

<110> SIRS-Lab GmbH

<120> Method of enriching/separating prokaryotic DNA by means of a protein which specifically binds DNA containing non-methylated CpG motifs

<130> Pat 3696/29-PCT

<140>
<141>

<160> 8

<170> PatentIn Ver. 2.1

<210> 1
<211> 543
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(561)

<400> 1

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ggt gga ggg cgc aag agg cct gtc cct gat cca aac ctg cag cgc cgg    48
Gly Gly Gly Arg Lys Arg Pro Val Pro Asp Pro Asn Leu Gln Arg Arg
  1               5                  10                  15

gca ggg tca ggg aca ggg gtt ggg gcc atg ctt gct cgg ggc tct gct    96
Ala Gly Ser Gly Thr Gly Val Gly Ala Met Leu Ala Arg Gly Ser Ala
             20                  25                  30

tcg ccc cac aaa tcc tct ccg cag ccc ttg gtg gcc aca ccc agc cag   144
Ser Pro His Lys Ser Ser Pro Gln Pro Leu Val Ala Thr Pro Ser Gln
         35                  40                  45

cat cac cag cag cag cag cag cag atc aaa cgg tca gcc cgc atg tgt   192
His His Gln Gln Gln Gln Gln Gln Ile Lys Arg Ser Ala Arg Met Cys
     50                  55                  60

ggt gag tgt gag gca tgt cgg cgc act gag gac tgt ggt cac tgt gat   240
Gly Glu Cys Glu Ala Cys Arg Arg Thr Glu Asp Cys Gly His Cys Asp
 65                  70                  75                  80

ttc tgt cgg gac atg aag aag ttc ggg ggc ccc aac aag atc cgg cag   288
Phe Cys Arg Asp Met Lys Lys Phe Gly Gly Pro Asn Lys Ile Arg Gln
                 85                  90                  95

aag tgc cgg ctg cgc cag tgc cag ctg cgg gcc cgg gaa tcg tac aag   336
Lys Cys Arg Leu Arg Gln Cys Gln Leu Arg Ala Arg Glu Ser Tyr Lys
            100                 105                 110

tac ttc cct tcc tcg ctc tca cca gtg acg ccc tca gag tcc ctg cca   384
Tyr Phe Pro Ser Ser Leu Ser Pro Val Thr Pro Ser Glu Ser Leu Pro
        115                 120                 125
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agg ccc cgc cgg cca ctg ccc acc caa cag cag cca cag cca tca cag   432
Arg Pro Arg Arg Pro Leu Pro Thr Gln Gln Gln Pro Gln Pro Ser Gln
    130                 135                 140

aag tta ggg cgc atc cgt gaa gat gag ggg gca gtg gcg tca tca aca   480
Lys Leu Gly Arg Ile Arg Glu Asp Glu Gly Ala Val Ala Ser Ser Thr
145                 150                 155                 160

gtc aag gag cct cct gag gct aca gcc aca cct gag cca ctc tca gat   528
Val Lys Glu Pro Pro Glu Ala Thr Ala Thr Pro Glu Pro Leu Ser Asp
                165                 170                 175

gag gac cta cct ctg                                              543
Glu Asp Leu Pro Leu
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<210> 2
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<212> PRT
<213> Homo sapiens

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Gly Gly Gly Arg Lys Arg Pro Val Pro Asp Pro Asn Leu Gln Arg Arg
  1               5                  10                  15

Ala Gly Ser Gly Thr Gly Val Gly Ala Met Leu Ala Arg Gly Ser Ala
            20                  25                  30

Ser Pro His Lys Ser Ser Pro Gln Pro Leu Val Ala Thr Pro Ser Gln
        35                  40                  45

His His Gln Gln Gln Gln Gln Gln Ile Lys Arg Ser Ala Arg Met Cys
    50                  55                  60

Gly Glu Cys Glu Ala Cys Arg Arg Thr Glu Asp Cys Gly His Cys Asp
65                  70                  75                  80

Phe Cys Arg Asp Met Lys Lys Phe Gly Gly Pro Asn Lys Ile Arg Gln
                85                  90                  95

Lys Cys Arg Leu Arg Gln Cys Gln Leu Arg Ala Arg Glu Ser Tyr Lys
            100                 105                 110

Tyr Phe Pro Ser Ser Leu Ser Pro Val Thr Pro Ser Glu Ser Leu Pro
        115                 120                 125

Arg Pro Arg Arg Pro Leu Pro Thr Gln Gln Gln Pro Gln Pro Ser Gln
    130                 135                 140

Lys Leu Gly Arg Ile Arg Glu Asp Glu Gly Ala Val Ala Ser Ser Thr
145                 150                 155                 160

Val Lys Glu Pro Pro Glu Ala Thr Ala Thr Pro Glu Pro Leu Ser Asp
                165                 170                 175

Glu Asp Leu Pro Leu
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<212> DNA
<213> Artificial sequence

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<223> Description of artificial sequence: Primer

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ctgaaggtag cattagtctt tgataacg 28